Figure 1A

```
  1  GGTCCGAGCGGGGGGAGGGGTGAGGGAGGGGTGGGGGTGGGGGGCTCCGGGGAAGGCGGT   60

 61  TGCAGCTCCTGAGTGCAGCCCGGCTTCCTGCCACTGTCCCGGCTCGGCCACCTCTCTGTC  120

121  ATGGCTCTGGCGGACAGCACACGTGGATTACCCAACGGGGGCGGCGGCGGGGGCGGCAGT  180
  1  M  A  L  A  D  S  T  R  G  L  P  N  G  G  G  G  G  G  G  S    20

181  GGCTCCTCGTCGTCCTCGGCGGAGCCACCGCTCTTCCCCGACATCGTGGAGCTGAACGTG  240
 21  G  S  S  S  S  S  A  E  P  P  L  F  P  D  I  V  E  L  N  V    40

241  GGGGGCCAGGTGTACGTGACCCGGCGCTGCACGGTGGTGTCGGTGCCCGACTCGCTGCTC  300
 41  G  G  Q  V  Y  V  T  R  R  C  T  V  V  S  V  P  D  S  L  L    60

301  TGGCGCATGTTCACGCAGCAGCAGCCGCAGGAGCTGGCCCGGGACAGCAAAGGCCGCTTC  360
 61  W  R  M  F  T  Q  Q  Q  P  Q  E  L  A  R  D  S  K  G  R  F    80

361  TTTCTGGACCGGGACGGCTTCCTCTTCCGCTACATCCTGGATTACCTGCGGGACTTGCAG  420
 81  F  L  D  R  D  G  F  L  F  R  Y  I  L  D  Y  L  R  D  L  Q   100

421  CTCGTGCTGCCCGACTACTTCCCCGAGCGCAGCCGGCTGCAGCGCGAGGCCGAGTACTTC  480
101  L  V  L  P  D  Y  F  P  E  R  S  R  L  Q  R  E  A  E  Y  F   120

481  GAGCTGCCAGAGCTCGTGCGCCGCCTCGGGGCGCCCCAGCAGCCCGGCCCGGGGCCGCCG  540
121  E  L  P  E  L  V  R  R  L  G  A  P  Q  Q  P  G  P  G  P  P   140

541  CCCTCGCGGCGCGGGGTGCACAAGGAGGGCTCGCTGGGTGACGAGCTGCTGCCGCTTGGC  600
141  P  S  R  R  G  V  H  K  E  G  S  L  G  D  E  L  L  P  L  G   160

601  TACTCGGAGCCCGAACAGCAGGAGGGCGCCTCTGCCGGGGCGCCGTCGCCCACGCTGGAG  660
161  Y  S  E  P  E  Q  Q  E  G  A  S  A  G  A  P  S  P  T  L  E   180

661  CTGGCTAGCCGCAGTCCGTCCGGGGGCGCGGCGGGCCCGCTGCTCACGCCGTCCCAGTCG  720
181  L  A  S  R  S  P  S  G  G  A  A  G  P  L  L  T  P  S  Q  S   200

721  CTGGACGGCAGCCGGCGCTCGGGCTACATCACCATCGGCTACCGCGGCTCCTACACCATC  780
201  L  D  G  S  R  R  S  G  Y  I  T  I  G  Y  R  G  S  Y  T  I   220

781  GGGCGGGACGCCCAGGCGGACGCCAAGTTCCGGCGGGTGGCGCACATCACCGTTGGCGGA  840
221  G  R  D  A  Q  A  D  A  K  F  R  R  V  A  H  I  T  V  G  G   240

841  AAGACGTTCCTGGCCAAGGAGGTGTTTGGGGACACCCTGAATGAAAGCCGGGACCCCGAC  900
241  K  T  F  L  A  K  E  V  F  G  D  T  L  N  E  S  R  D  P  D   260
```

Figure 1B

```
901   CGTCCTCCGGAGCGCTACACTAGCCGCTATTACCTCAAGTTCAATTTCCTGGAGCAGGCT   960
261   R  P  P  E  R  Y  T  S  R  Y  Y  L  K  F  N  F  L  E  Q  A     280

961   TTCGACAAGCTGTCCGAGTCGGGCTTCCACATGGTGGCGTGCAGCTCCACGGGCACCTGC   1020
281   F  D  K  L  S  E  S  G  F  H  M  V  A  C  S  S  T  G  T  C     300

1021  GCCTTTGCCAGCAGCACCGACCAGAGCGAGGACAAGATCTGGACCAGCTACACCGAGTAC   1080
301   A  F  A  S  S  T  D  Q  S  E  D  K  I  W  T  S  Y  T  E  Y     320

1081  GTCTTCTGCAGGGAGTGAGCTTCCCAGACCCCCTCGCCACTCCAGCGCCCAGTCCTTCTC   1140
321   V  F  C  R  E                                                  325

1141  CTGCCCGAGAGATGATTACAGAGCCTCTTGTCCCACCTTTGTCCCCTGGCTGCTGCCCTC   1200

1201  CCATTCTCCCCCTCCAGTAGTAGCTGGGTGAGACCTGTCCGCCCCACCTTCCCTCCACTAC   1260

1261  AGAACCTGCAGCCGCAAATCCTCTGGGCTGCTTCGTCTTCTTTGGACCTCCTGAACCGAG   1320

1321  AGAACCCAGAGGAACCCCCACCCCACCCCCACCTACCACTCCATGCTTTCTCTACTCCCT   1380

1381  GCCTCAAACCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGGAGTGTGGC   1440

1441  CACAGACCGGGGGATGATTGAATTGTTCAGAACCTGATTGGACCGTGTCCAATGTGCGGA   1500

1501  AGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAGATCAGGAT   1560

1561  TGGTTCCACTGTCTGGGGTTAGTGTTTTACAAGGTCATTACACAGTCTTTTTGACCTCTT   1620

1621  TTGAAGGTAGAGTTTTAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAGGACCCCAT   1680

1681  GGAGGCAGTCCTCAAACCACCCCTCCCCCAGATGGTACTTCAGTTTGGATCTATTGGGGG   1740

1741  AGTGTGGCCACAGACCGGGGGATGATTGAATTGTTCAGAACCTGATTGGACCGTGTCCAA   1800

1801  TGTGCGGAAGATTTCCTTGAAATCTTCTCAAGCTCTTATGACTCACTGGGGGTTTAAGAG   1860

1861  ATCAGGATTGGTTCCACTGTCTGGGGTTAGTGTTTTACAAGGTCATTACACAGTCTTTTT   1920

1921  GACCTCTTTTGAAGGTAGAGTTTTAGAAGGCTGGATGGAAGATTCTGAGCCTGGAATTAG   1980
```

Figure 1C

1081 GA[illegible]ATGGAGGCAGCTCAGTAACTAAACTAATAAAGTTTTGAAAAGTTACA[illegible]GTAAAA 1140

1141 AAAAAAAAAAAA 1152

Figure 2A

```
                         1                                                 51
K+betaM6           (1)   MALALLTPSLPNSSSSSSSSSSSSSSAEPPLFPDIVELNVGGQVYVTRRC
KCNMB1             (1)   -----------MVKKLVMA-HRRETRALLLGVTMVVCAVITYYILVTTVL
K+Hnov27           (1)   --  MSRRLITRSPASPLKN-SIPTPAVLTHNNAPVHIDVGGHMYTSSLA
K+Hnov28           (1)   ---------------------MDNSDWSSTMTDPVTLNVGGHLYTTSLT
KIAA1317           (1)   ---...KKSTMALSSNNTPYYPPEGSSAVPNSFPEVVELNVGGQVYFTRHS
CG10465            (1)   ----------------MSENMSSDHKILLKGHSSQYLFLNVGGHLYYTTIG
CG10830            (1)   ---------------------------------MPEIIELNVGGVSYTTTLA
K+channel_tetra    (1)   ------------------------------MTSVEDVITLNVGGTMYTTTRS

                         51                                                100
K+betaM6           (51)  TVVSVPDSLLWRMFTQQ----QPQELARDSKGRFFLDRDGFLFRYILDYL
KCNMB1             (40)  PLYQKSVWTQESKCHLIETNIRDQEELKGKKVPQYPCLWVNVSAAGRWAV
K+Hnov27           (47)  TLTKYPESRIGRLFDGTEP-----IVLDSLKQHYFIDRDGQMFRYILNFL
K+Hnov28           (29)  TLTRYPDSMLGAMFGGDFP------TARDPQGNYFIDRDGPLFRYVLNFL
KIAA1317           (49)  TLISIPHSLLWKMFSPKR--DTANDLAKDSKGRFFIDRDGFLFRYILDYL
CG10465            (36)  TLTKNNDTMLSAMFSGR------MEVLTDSEGWILIDRCGNHFGIILNYL
CG10830            (20)  TLLQDKSTLLAELFGEG-----RDSLAKDSKGRYFLDRDGVLFRYILDFL
K+channel_tetra    (23)  TLSKETDTLLANIASGSLSEDEQANVVTLPDGTLFVDRDGPLFAYVLHFL

                         101                                               150
K+betaM6           (97)  RDLQLVLPDYFPERSRLQREAEYFELPELVRRLGAPQQPGPGPPPSRRGV
KCNMB1             (90)  LYHTEDTRDQNQQCSYIPGSVDNYQTAPADVEKVRAKFQEQQ--------
K+Hnov27           (92)  RTSKLLIPDDFKDYTLLYEEAKYFQLQPMLLEMERWKQDRET--------
K+Hnov28           (73)  RTSELTLPLDFKEFDLLRKEADFYQIEPLIQCLNDPKPLYP---------
KIAA1317           (97)  RDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS--P------
CG10465            (80)  RDGTVPLPETNKEIAELLAEAKYYCITELAISCERALYAHQEPKPICRIP
CG10830            (65)  RDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSERDARP---------
K+channel_tetra    (73)  RTDKLSLPEQFREVARLKDEADFYRLERFSTLLSNASSISP---------

                         151                                               200
K+betaM6           (147) HKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGAAGPLLT
KCNMB1             (132) --------------------------------------------------
K+Hnov27           (134) --------------------------------------------------
K+Hnov28           (114) --------------------------------------------------
KIAA1317           (139) -------DEFCHSDFEDASQ---------------------GSDTRICP
CG10465            (130) LITSQKEEQLLLSVSLKPAVILVVQRQNN-------------KYSYTSTS
CG10830            (106) ----------------------------P---------------------
K+channel_tetra    (114) -------------------------------------------RPRTANG

                         201                                               250
K+betaM6           (197) PSQSLDGSRRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAK
KCNMB1             (132) --------VFYCFSAPRGNETSVLFQRLYGPQALLFSLFWPTFLLTGGLL
K+Hnov27           (134) -----------GRFSRPCECLVVRVAPDLGERITLSGDKSLIEEVFPEIG
K+Hnov28           (114) ----------MDTFEEVVELSSTRKLSKYSNPVAVIITQLTITTKVHSLL
KIAA1317           (160) PSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAK
CG10465            (167) DDNLLKNIELFDKLSLRFNERILFIKDVIGPSEICCWSFYGHGKKVAEVC
CG10830            (107) -----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCR
K+channel_tetra    (121) YNTITSGAETGGYITLGYRG------------------------------

                         251                                               300
K+betaM6           (247) EVFGDTLNESRDPDRP-PERYTSRYYLKFNFLEQAFDKLSESGFHMVACS
KCNMB1             (174) IIAMVKSNQYLSILAAQK--------------------------------
K+Hnov27           (173) DVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQVLERLQ-QRGFEIVGSC
K+Hnov28           (154) EGISNYFTKWNKHMMDTRDCQVSFTFGPCDYHQEVSLRVHLMEYITKQGF
KIAA1317           (210) EVFGETLNESRDPDRA-PERYTSRFYLKFKHLERAFDMLSECGFHMVACN
CG10465            (217) CTSIVYATDRKHTKVEFPEARIYEETLQVLLYENRNAPDQELMQATSSAR
CG10830            (146) EVFGDTLNECRDPDHGHTDRYTSRFFLKHHYIEQAFDNLHDHGYRMAGSC
K+channel_tetra    (141) --------------------------------------------------
```

Figure 2B

```
                           301                                              350
         K+betaM6    (296) STRIITAFALT- -L,SEDKINTSYIHYVFDRE-----------------
           KCNMB1    (192) --------------------------------------------------
         K+Hnov27    (222) GGSVDSSQFLHYVLRREIRRIPPVPVVIFIKQEPL---------------
         K+Hnov28    (214) TIFNIFVHHMQKFANHNTVEHNWTF RLARKTDI----------------
         KIAA1317    (259) SDVTASFIN- - --QYTDDKIWSSYTEYVFYREPLFNNIPSHSL TQKNGK
          CG10465    (267) VGAASGTSIN,YTSDEEEERTGLARLRSNKRNNPQ----------------
          CG10830    (196) GSGTAGSAAEPKPGVDTEENRWNHYNEFVFIRD-----------------
K+channel_tetra    (141) --------------------------------------------------

                           351                                              400
         K+betaM6    (326) --------------------------------------------------
           KCNMB1    (192) --------------------------------------------------
         K+Hnov27    (257) --------------------------------------------------
         K+Hnov28    (238) --------------------------------------------------
         KIAA1317    (304) GDKEGESGTQCNDLSTSSTDSQSEASSPQETVIQGPVTRQTNIQTLDRPI
          CG10465    (302) --------------------------------------------------
          CG10830    (229) --------------------------------------------------
K+channel_tetra    (141) --------------------------------------------------

                           401                                              450
         K+betaM6    (326) --------------------------------------------------
           KCNMB1    (192) --------------------------------------------------
         K+Hnov27    (257) --------------------------------------------------
         K+Hnov28    (238) --------------------------------------------------
         KIAA1317    (354) KKGPVQLIQQSEMRRKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELE
          CG10465    (302) --------------------------------------------------
          CG10830    (229) --------------------------------------------------
K+channel_tetra    (141) --------------------------------------------------

                           451                            482
         K+betaM6    (326) --------------------------------
           KCNMB1    (192) --------------------------------
         K+Hnov27    (257) --------------------------------
         K+Hnov28    (238) --------------------------------
         KIAA1317    (404) KCIQDFLKIKIPDRFPERKHPWQSELLRKYHL
          CG10465    (302) --------------------------------
          CG10830    (229) --------------------------------
K+channel_tetra    (141) --------------------------------
```

Figure 3

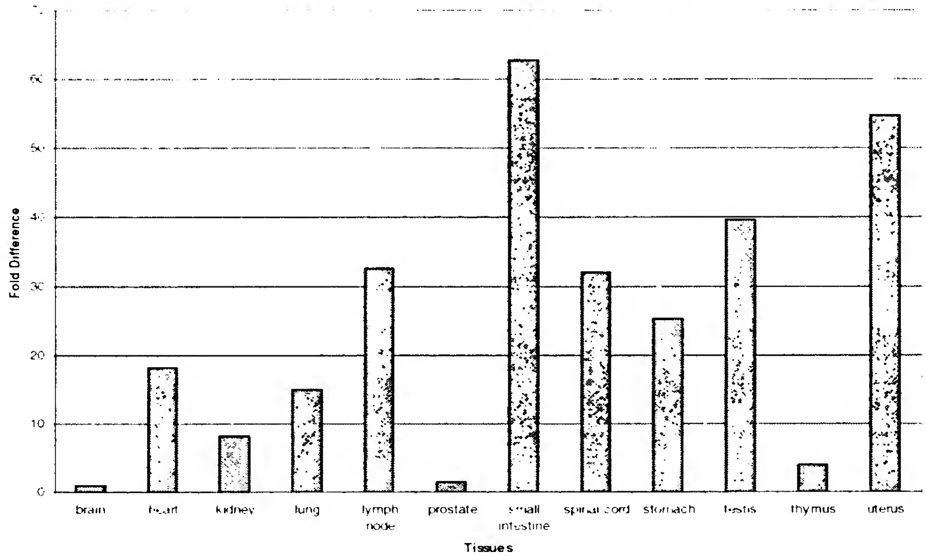
Fold Difference
0
10
20
30
40
50
60
brain
heart
kidney
lung
lymph node
prostate
small intestine
spinal cord
stomach
testis
thymus
uterus
Tissues

Figure 4.

Protein	Genbank / SWISS-PROT Accession No.	Identities	Similarities
human Maxi-K potassium channel beta subunit, KCNMB1 protein	gi|4758625	0.0%	37.5%
human potassium channel K+Hnov27 protein	gi|Y34125	30.21%	39.15%
human potassium channel K+Hnov28 protein	gi|Y34129	30.04%	38.63%
Caenorhabditis elegans K+ channel tetramerisation domain containing protein	gi|3880445	31.11%	39.26%
Drosophila CG10465 protein	gi|17946205	23.9%	33.0%
Drosophila CG10830 protein	gi|7300672	50.89%	62.5%
human KIAA1317 protein	gi|7243015	60.42%	69.97%

Figure 5